

0590  
1026

#2

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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/977,653

DATE: 11/01/2001

TIME: 10:48:36

Input Set : A:\MA-702D2.ST25.txt

Output Set: N:\CRF3\11012001\I977653.raw

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3 <110> APPLICANT: Thompson, Mark  
 4 Knuth, Mark  
 5 Cardineau, Guy  
 7 <120> TITLE OF INVENTION: Bacillus thuringiensis Toxins with Improved Activity  
 9 <130> FILE REFERENCE: MA-702D2  
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/977,653  
 C--> 11 <141> CURRENT FILING DATE: 2001-10-15  
 11 <150> PRIOR APPLICATION NUMBER: US 09/222,594  
 12 <151> PRIOR FILING DATE: 1998-12-28  
 14 <150> PRIOR APPLICATION NUMBER: US 08/904,278  
 15 <151> PRIOR FILING DATE: 1998-07-31  
 17 <160> NUMBER OF SEQ ID NOS: 10  
 19 <170> SOFTWARE: PatentIn version 3.1  
 21 <210> SEQ ID NO: 1  
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 23 <212> TYPE: DNA  
 24 <213> ORGANISM: Bacillus thuringiensis  
 26 <400> SEQUENCE: 1

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31	aaacaagaat	gggctacgat	tggagcatat	attcagactg	gattagggtt	accagtaaat	180
33	gaacaacaat	taagaacaca	tgtaatttta	agtcaggata	tatcaatacc	tagtgatttt	240
35	tctcaattat	atgatgttta	ttgttctgat	aaaacttcag	cagaatgggtg	gaataaaaaat	300
37	ttatatcctt	taattattaa	atctgctaata	gatattgctt	catatgggtt	taaagttgct	360
39	ggtgatcctt	ctattaagaa	agatggatat	tttaaaaaat	tgcaagatga	attagataat	420
41	attgttgata	ataattccga	tgatgatgca	atagctaaag	ctattaaaga	ttttaaagcg	480
43	cgatgtggta	ttttaattaa	agaagctaaa	caatatgaag	aagctgcaaa	aaatattgta	540
45	acatcttttag	atcaattttt	acatgggtgat	cagaaaaaat	tagaagggtg	tatcaatatt	600
47	caaaaacggt	taaaagaagt	tcaaacagct	cttaatcaag	cccatgggga	aagtagtcca	660
49	gctcataaag	agttattaga	aaaagtaaaa	aattttaaaaa	caacattaga	aaggactatt	720
51	aaagctgaac	aagattttaga	gaaaaaagta	gaatatagtt	ttctattagg	accattgtta	780
53	ggatttggtg	tttatgaaat	tcttgaaaat	actgctgttc	agcatataaa	aatcaaat	840
55	gatgagataa	agaaacaatt	agattctgct	cagcatgatt	tggatagaga	tgttaaaatt	900
57	ataggaatgt	taaatagtat	taatacagat	attgataatt	tatatagtca	aggacaagaa	960
59	gcaattaaag	ttttccaaaa	gttacaaggt	atttgggcta	ctattggagc	tcaaatagaa	1020
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63	attgaacttg	aggacgcttc	tgatgcttgg	ttagttgtgg	ctcaagaagc	tcgtgatttt	1140
65	acactaaatg	cttattcaac	taatagtaga	caaaattttac	cgattaatgt	tatatcagat	1200
67	tcatgtaatt	gttcaacaac	aaatatgaca	tcaaatcaat	acagtaatcc	aacaacaaat	1260
69	atgacatcaa	atcaatatat	gatttcacat	gaatatacaa	gtttaccaa	taattttatg	1320
71	ttatcaagaa	atagtaattt	agaatataaa	tgtcctgaaa	ataattttat	gatataattg	1380
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79	<213>	ORGANISM: Bacillus thuringiensis					
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84 1 5 10 15
87 Thr Ile Lys Leu Asn Ser Asn Lys Lys Tyr Gly Pro Gly Asp Met Thr
88 20 25 30
91 Asn Gly Asn Gln Phe Ile Ile Ser Lys Gln Glu Trp Ala Thr Ile Gly
92 35 40 45
95 Ala Tyr Ile Gln Thr Gly Leu Gly Leu Pro Val Asn Glu Gln Gln Leu
96 50 55 60
99 Arg Thr His Val Asn Leu Ser Gln Asp Ile Ser Ile Pro Ser Asp Phe
100 65 70 75 80
103 Ser Gln Leu Tyr Asp Val Tyr Cys Ser Asp Lys Thr Ser Ala Glu Trp
104 85 90 95
107 Trp Asn Lys Asn Leu Tyr Pro Leu Ile Ile Lys Ser Ala Asn Asp Ile
108 100 105 110
111 Ala Ser Tyr Gly Phe Lys Val Ala Gly Asp Pro Ser Ile Lys Lys Asp
112 115 120 125
115 Gly Tyr Phe Lys Lys Leu Gln Asp Glu Leu Asp Asn Ile Val Asp Asn
116 130 135 140
119 Asn Ser Asp Asp Asp Ala Ile Ala Lys Ala Ile Lys Asp Phe Lys Ala
120 145 150 155 160
123 Arg Cys Gly Ile Leu Ile Lys Glu Ala Lys Gln Tyr Glu Glu Ala Ala
124 165 170 175
127 Lys Asn Ile Val Thr Ser Leu Asp Gln Phe Leu His Gly Asp Gln Lys
128 180 185 190
131 Lys Leu Glu Gly Val Ile Asn Ile Gln Lys Arg Leu Lys Glu Val Gln
132 195 200 205
135 Thr Ala Leu Asn Gln Ala His Gly Glu Ser Ser Pro Ala His Lys Glu
136 210 215 220
139 Leu Leu Glu Lys Val Lys Asn Leu Lys Thr Thr Leu Glu Arg Thr Ile
140 225 230 235 240
143 Lys Ala Glu Gln Asp Leu Glu Lys Lys Val Glu Tyr Ser Phe Leu Leu
144 245 250 255
147 Gly Pro Leu Leu Gly Phe Val Val Tyr Glu Ile Leu Glu Asn Thr Ala
148 260 265 270
151 Val Gln His Ile Lys Asn Gln Ile Asp Glu Ile Lys Lys Gln Leu Asp
152 275 280 285
155 Ser Ala Gln His Asp Leu Asp Arg Asp Val Lys Ile Ile Gly Met Leu
156 290 295 300
159 Asn Ser Ile Asn Thr Asp Ile Asp Asn Leu Tyr Ser Gln Gly Gln Glu
160 305 310 315 320
163 Ala Ile Lys Val Phe Gln Lys Leu Gln Gly Ile Trp Ala Thr Ile Gly
164 325 330 335
167 Ala Gln Ile Glu Asn Leu Arg Thr Thr Ser Leu Gln Glu Val Gln Asp
168 340 345 350
171 Ser Asp Asp Ala Asp Glu Ile Gln Ile Glu Leu Glu Asp Ala Ser Asp
172 355 360 365
175 Ala Trp Leu Val Val Ala Gln Glu Ala Arg Asp Phe Thr Leu Asn Ala
176 370 375 380
179 Tyr Ser Thr Asn Ser Arg Gln Asn Leu Pro Ile Asn Val Ile Ser Asp

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180 385          390          395          400
183 Ser Cys Asn Cys Ser Thr Thr Asn Met Thr Ser Asn Gln Tyr Ser Asn
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187 Pro Thr Thr Asn Met Thr Ser Asn Gln Tyr Met Ile Ser His Glu Tyr
188          420          425          430
191 Thr Ser Leu Pro Asn Asn Phe Met Leu Ser Arg Asn Ser Asn Leu Glu
192          435          440          445
195 Tyr Lys Cys Pro Glu Asn Asn Phe Met Ile Tyr Trp Tyr Asn Asn Ser
196          450          455          460
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200 465          470          475
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205 <212> TYPE: DNA
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213 aagcaagaat gggccacgat tggcgcatatc attcagactg gactcggctt accagtgaat      180
215 gagcaacagc tgagaaccca cgttaacctt agtcaagaca tcagcatacc atctgacttt      240
217 tctcaactct acgatgtgta ttgttctgac aagactagtg cagaatggtg gaacaagaat      300
219 ctctatcctt tgatcatcaa gtctgccaat gacattgctt catatggttt caaagttgct      360
221 ggtgatcctt cgatcaagaa agatggttac ttcaagaagc ttcaagatga actcgacaac      420
223 attgttgaca acaactccga cgacgatgcg atagccaaag ccatcaagga cttcaaagca      480
225 agatgtggca ttctcatcaa ggaagccaag cagtatgaag aagctgccaa gaacattgta      540
227 acatcattgg atcagtttct ccatggagac cagaagaagc tcgagggtgt catcaacatt      600
229 cagaaacgtc tgaaagaggt tcaaacagct ctgaatcaag cccatgggga atccagtcca      660
231 gctcacaag agcttcttga gaaagtgaag aacttgaaga ccacacttga gaggaccatc      720
233 aaagctgaac aagacttggg gaagaaagta gagtacagct ttctacttgg acccttgta      780
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247 aactgaatg cctactcaac caacagtcga cagaatctcc cgatcaatgt gatctcagat     1200
249 tcatgcaatt gctccaccac caacatgaca tccaatcagt acagcaatcc aacaaccaac     1260
251 atgactagca atcagtacat gattagccat gagtatacca gcttgcccaa caacttcatg     1320
253 ttgtcaagga attcgaacct ggagtacaag tgccctgaga acaacttcat gatctactgg     1380
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278          50          55          60
281 Arg Thr His Val Asn Leu Ser Gln Asp Ile Ser Ile Pro Ser Asp Phe
282 65          70          75          80
285 Ser Gln Leu Tyr Asp Val Tyr Cys Ser Asp Lys Thr Ser Ala Glu Trp
286          85          90          95
289 Trp Asn Lys Asn Leu Tyr Pro Leu Ile Ile Lys Ser Ala Asn Asp Ile
290          100         105         110
293 Ala Ser Tyr Gly Phe Lys Val Ala Gly Asp Pro Ser Ile Lys Lys Asp
294          115         120         125
297 Gly Tyr Phe Lys Lys Leu Gln Asp Glu Leu Asp Asn Ile Val Asp Asn
298          130         135         140
301 Asn Ser Asp Asp Asp Ala Ile Ala Lys Ala Ile Lys Asp Phe Lys Ala
302 145          150          155         160
305 Arg Cys Gly Ile Leu Ile Lys Glu Ala Lys Gln Tyr Glu Glu Ala Ala
306          165          170         175
309 Lys Asn Ile Val Thr Ser Leu Asp Gln Phe Leu His Gly Asp Gln Lys
310          180         185         190
313 Lys Leu Glu Gly Val Ile Asn Ile Gln Lys Arg Leu Lys Glu Val Gln
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317 Thr Ala Leu Asn Gln Ala His Gly Glu Ser Ser Pro Ala His Lys Glu
318          210         215         220
321 Leu Leu Glu Lys Val Lys Asn Leu Lys Thr Thr Leu Glu Arg Thr Ile
322 225          230         235         240
325 Lys Ala Glu Gln Asp Leu Glu Lys Lys Val Glu Tyr Ser Phe Leu Leu
326          245         250         255
329 Gly Pro Leu Leu Gly Phe Val Val Tyr Glu Ile Leu Glu Asn Thr Ala
330          260         265         270
333 Val Gln His Ile Lys Asn Gln Ile Asp Glu Ile Lys Lys Gln Leu Asp
334          275         280         285
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338          290         295         300
341 Asn Ser Ile Asn Thr Asp Ile Asp Asn Leu Tyr Ser Gln Gly Gln Glu
342 305          310         315         320
345 Ala Ile Lys Val Phe Gln Lys Leu Gln Gly Ile Trp Ala Thr Ile Gly
346          325         330         335
349 Ala Gln Ile Glu Asn Leu Arg Thr Thr Ser Leu Gln Glu Val Gln Asp
350          340         345         350
353 Ser Asp Asp Ala Asp Glu Ile Gln Ile Glu Leu Glu Asp Ala Ser Asp
354          355         360         365
357 Ala Trp Leu Val Val Ala Gln Glu Ala Arg Asp Phe Thr Leu Asn Ala
358          370         375         380
361 Tyr Ser Thr Asn Ser Arg Gln Asn Leu Pro Ile Asn Val Ile Ser Asp
362 385          390         395         400
365 Ser Cys Asn Cys Ser Thr Thr Asn Met Thr Ser Asn Gln Tyr Ser Asn
366          405         410         415
369 Pro Thr Thr Asn Met Thr Ser Asn Gln Tyr Met Ile Ser His Glu Tyr

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370          420          425          430
373 Thr Ser Leu Pro Asn Asn Phe Met Leu Ser Arg Asn Ser Asn Leu Glu
374          435          440          445
377 Tyr Lys Cys Pro Glu Asn Asn Phe Met Ile Tyr Trp Tyr Asn Asn Ser
378          450          455          460
381 Asp Trp Tyr Asn Asn Ser Asp Trp Tyr Asn Asn
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395 cagactggac tcggcttacc agtgaatgag caacagctga gaacccacgt taaccttagt      180
397 caagacatca gcataccatc tgacttttct caactctacg atgtgtattg ttctgacaag      240
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409 aagaagctcg aggggtgcat caacattcag aaacgtctga aagaggttca aacagctctg      600
411 aatcaagccc atgggggaatc cagtccagct cacaaagagc ttcttgagaa agtgaagaac      660
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423 tggggccacta ttggagctca gatagagaat cttcgcacca cgtcccttca agaagtccaa      1020
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427 gttgtggctc aagaagctcg tgacttcaca ctgaatgcct actcaaccaa cagtcgacag      1140
429 aatctccoga tcaatgtgat ctcagattca tgcaattgct ccaccaccaa catgacatcc      1200
431 aatcagtaca gcaatccaac aaccaacatg actagcaatc agtacatgat tagccatgag      1260
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441 <400> SEQUENCE: 6
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447 Pro Gly Asp Met Thr Asn Gly Asn Gln Phe Ile Ile Ser Lys Gln Glu
448          20          25          30
451 Trp Ala Thr Ile Gly Ala Tyr Ile Gln Thr Gly Leu Gly Leu Pro Val
452          35          40          45
455 Asn Glu Gln Gln Leu Arg Thr His Val Asn Leu Ser Gln Asp Ile Ser
456          50          55          60
459 Ile Pro Ser Asp Phe Ser Gln Leu Tyr Asp Val Tyr Cys Ser Asp Lys
460 65          70          75          80

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L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date